

SEULBERGER et al.,

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AMENDMENTS TO THE SPECIFICATION

Please amend paragraph 6, on page 23 of the specification as followed:

Example 3

Homology comparison of the HvSD36 protein sequence SEQ ID NO: 2

A comparison of the HvSD36 protein sequence with protein sequences in the database revealed homologies to the following protein sequences known to date:

Please amend paragraph 1, on page 26 of the specification as followed:

SEQ ID NO: 2	HPPD_Hv	510	520	530	540	550
		SE LFK-SIE-DY	--EKS	LEA KQSAAV-QGS		
HPPD_Ath		SE LFK-SIE-DY	--EKT	LEA KQLVG		
HPPD_HUMAN		NS LFK-APEKEQ	--ELRGMLTH	METNGVVPGM		
HPPD_RAT		NS LFK-APEKEQ	--ALRG			
HPPD_PIG		NS LFK-APEKEQ	--ELRGMLTD	TDPNGVPPRL		
HPPD_MOUSE		NS LFK-APEKEQ	--ALRGMLTD	LEPNGVRSCH		
HPPD_PSESP		KA LFK-SIERDQ	--VRRGVLT	-D		
MELA_SHECO		KA LFK-SIERDQ	--VRRGVL			
PEA3_MOUSE		VYKPVCEPEA	LPSLAFFDQ	RPALKAEFD	FVSEEDTVPL	SHLDESPTAL

	560	570
HPPD_Hv		
HPPD_Ath		
HPPD_HUMAN		
HPPD_RAT		
HPPD_PIG		
HPPD_MOUSE		
HPPD_PSESP		
MELA_SHECO		
PEA3_MOUSE		PELTGPAPPF GHRGGYST

Key:

HPPD_Hv: *Hordeum vulgare* 4-hydroxyphenylpyruvate dioxxygenase (HvSD36) SEQ ID NO: 2
HPPD_Ath: *Arabidopsis thaliana* 4-hydroxyphenylpyruvate dioxxygenase
HPPD_HUMAN: *H.sapiens* 4-hydroxyphenylpyruvate dioxxygenase
HPPD_PIG: pig 4-hydroxyphenylpyruvate dioxxygenase
HPPD_RAT: rat P alloantigen
HPPD_MOUSE: mouse 4-hydroxyphenylpyruvate dioxxygenase
MELA_SHECO: *S. colwelliana* mela protein
HPPD_PSESP: *Pseudomonas* sp. (strain P.J.874) 4-hydroxyphenylpyruvate dioxxygenase
PEA3_MOUSE: *Mus musculus* (mouse) PEA3 polypeptide

The greatest homology was with the *Arabidopsis* sequence, viz. 58% over the entire sequence (62% over 412 amino acids), followed by HPPD_RAT with 35% (over 365 amino acids), HPPD_HUMAN 34% (over 365 amino acids), HPPD_MOUSE 34% (over 371 amino acids).

Please amend paragraph 1-5, on page 25 of the specification as followed:

SEQ ID NO: 2

HFPD_EV
 HFPD_Ath
 HFPD_HUMAN
 HFPD_RAT
 HFPD_PIG
 HFPD_MOUSE
 HFPD_PSESP
 MELA_SHECO
 PEAS_MOUSE

260	270	280	290	300
VFFLPGFBNV	THPDA----	VDFGLTRFDH	VVGWVP--EL	-AFAAAYIAG
SEFLPGFERNV	EDASSF--P	LOYGIRHLDH	AVGNVP--EL	-GPALTYVAG
GQFLPGYRAP	AFMDPILLPKL	PKCSLEMDH	IVGHPQDQEN	--VSASEW----
GRFLPGFRAP	TYKDTLLPKL	PSCHLEIIDE	IVGHPQDQEN	--ESASEW----
LDSRPQPSQT	LLHRLLSKL	PKCGLEIIDE	IVGHPQDQEN	--ESASEW----
GRFLPGFRAP	TYKDTLLPKL	PKCHLEIIDE	IVGHPQDQEN	--QSASEW----
IDFV--PLGG	VDRHPVGA--	--GLKIIDE	LTHNVYRGRN	-A--YWAMP
SDF-----EA	LDRPTITQ--	-EKGFLIEVDH	LTHNVHGTTH	-E--YWSHF
HGTLGRHSSV	FQGPVMDCHS	FTSPQGGGRS	PLPAPYQROL	SEPCFPYPQO

SEQ ID NO: 2

HPPD_Hv
HPPD_Ath
HPPD_HUMAN
HPPD_RAT
HPPD_PIG
HPPD_MOUSE
HPPD_PSESP
NELA_SHECO
PEAS_MOUSE

310	320	330	340	350
FT—GFHF	AEFTADVG	TESGLNEVUL	ANMERGVLLP	LNEFVGCTKR
FT—GFHF	AEFTADVG	AEGLNEAVL	ASHDENVLLP	INEFVGCTKR
XLNLOFH	WEVDOTQVT	EYSGLRSIV	ANYESIRMP	INEPAPG-KK
XLNLOFH	WEVDOTQVT	EYSGLRSIV	ANYESIRMP	INEPAPG-RK
XLNLOFH	WEVDOTQVT	EYSGLRSIV	ANYESIRMP	INEPAPG-KK
XLNLOFH	WEVDOTQVT	EYSGLRSIV	ANYESIRMP	INEPAPG-KK
YKLFPHFI	RYF—DIEG	EYGLTSKAM	TAFDGHRI	LNE—ESSK
YKDFGFTSV	RYF—DIEG	SYTALISIAL	RSPDGSFCIP	INE—GKGD
WFKQ—SYHF	LYEQAGOPAS	SQGGVSGHRT	PGAGVVIROS	RYDFAYOSD

SEQ ID NO: 2

HPPD_EV
HPPD_Ath
HPPD_HUMAN
HPPD_RAT
HPPD_PIC
HPPD_MOUSE
HPPD_PSESP
MELA_SHECO
PRA3_MOUSE

360	370	380	390	400
RSQIQTFLEH	HGGPGVQH-I	AVASSDVLT	LREMRARM	GGPDTLEFFL
RSQIQTFLEH	NEGAMLOH-L	ALMHEDITAT	LREMRKRSSI	GGPDMFSPFP
RSQIQEYVDY	HGGAGVQH-I	ALKTEDIITA	IRHLER	—GUEFLSVF—
RSQIQEYVDY	HGGAGVQH-I	ALKTEDIITP	IRHLER	—GUEFLAVP—
RSQIQEYVDY	HGGAGVQH-I	ALKTEDIITA	IRHLER	—GUEFLAVP—
RSQIQEYVDY	HGGAGVQH-I	ALKTEDIITA	IRHLER	—GUEFLAVP—
AGQIEEFLNQ	FGGEGION-V	AFESDOLIKT	WHLKSI	—GKSTIAFF—
RWDIDEYLKE	YDGGVQH-L	AFHSRDIVAS	LDAMGGS	—SIGTLDIIP
PGCASHLEP	EGFSGSPGD	GVNCTGYERS	LAPPDVCII	VPKVEGGDI

SEQ ID NO: 2

HPPD_EV
HPPD_Ath
HPPD_HUMAN
HPPD_RAT
HPPD_PIG
HPPD_MOUSE
HPPD_PSESP
MELA_SHECO
FRA3_MOUSE

410	420	430	440	450
PXYTGVRRL	AGD--VLSEA	QINBCQELCV	LVDREDDG	--VLL--
PXYQELKER	VGD--VLSDD	QINCEKELGI	LVDREDDG	--VLL--
SYTTEQLREK	LATAKIVKE	NIDALSELKI	LVDYDERG	--VLL--
SSYTELLEN	LATSIQVKE	NHDVLSHLKI	LVDYDERG	--VLL--
PXYTQLORE	LSASIRVKE	SIDVLEELKI	LVDYDERG	--VLL--
SSYTLALRE	LSAKIQVKE	SNQVLEELKI	LVDYDERG	--VLL--
DTYTELNGR	LPH--HGE	PVGHQIANGI	LLDGSSSGD	KULL--
E-YTDIFER	LPG--VTE	DRDRIKHQI	LVDGDHDG	--VLL--
QEGIGAFREB	PPTQR--	-RGALQELMOF	LYALLDSTN	ABPTANTGEG

SEQ ID NO: 2

HPFD_HV
HPFD_Ath
HPFD_HUMAN
HPFD_RAT
HPFD_PIG
HPFD_MOUSE
HPFD_PSESP
MLA_SHECO
FRA3_MOUSE

460	470	480	490	500
QIFTPVGDR	PTLFLENIOR	IGCHMKDERG	KE---YQSG	OCGGFGKGNF
QIFTPFGDR	PTIFLEIIOR	VGCHMKDERG	KA---YQSG	OCGGFGKGNF
QIFTPVQDR	PTLFLEVIOR	HNEQ-----	-----	---GFGAGNF
QIFTPHQDR	PTLFLEVIOR	HNEQ-----	-----	---GFGAGNF
QIFTPHQDR	PTVFLEVIOR	HNEQ-----	-----	---GFGAGNF
QIFTPHQDR	PTLFLEVIOR	HNEQ-----	-----	---GFGAGNF
QIFSETLNGP	---VFTEIOR	---KGDD-----	-----	---GFGAGNF
QIFTKNLFGP	---IFTEIOR	---KHL-----	-----	---GFGAGNF
NEFKLIEPEE	VARLNGIQRM	RPAMWYDKLS	BSLRYYYEKG	INOKVAGHRY

Please amend paragraph 1-5, on page 24 of the specification as followed:

SEQ ID NO: 2		10	20	30	40	50
HPPD_Hv	MP	PTPTTFAATG
HPPD_AthMCHQAA	VSEWQHDDG
HPPD_HUMAN
HPPD_RAT
HPPD_PIG
HPPD_MOUSE
HPPD_PSESP
MELA_SHECO
PEA3_MOUSE	MTKSSNHCL	LRPENKPLN	GPGAQAASLR	PSPATLVSS	PGHAEPFPA	

SEQ ID NO: 2		60	70	80	90	100
HPPD_Hv	AAAAVTPEHA	RPHRMVRFP	RSDRFTLSF	HEVEFWCADA	ASAGRFAPA	
HPPD_Ath	AASPGKLV	GPSKVRKMP	KSDKFKVRK	HEVEFWCGDA	THVARRFSWG	
HPPD_HUMAN	M	TTYSKGAKE	ERGRFLH-F	ESVTFWVGH	KQAASFYCSK	
HPPD_RAT		IWDEKQPK	ERGRFLH-F	ESVTFWVGH	KQAASFYCHK	
HPPD_PIG	M	TSYSDKGEK	ERGRFLH-F	ESVTFWVGH	KQAASFYCHK	
HPPD_MOUSE	M	TYTHKGPKE	ERGRFLH-F	ESVTFWVGH	KQAASFYCHK	
HPPD_PSESP			ADLYEM	MGLKGFPIE	LASPTFWLE	
MELA_SHECO			MASEQNP	LGLLGIEFTS	FATPDLPHE	
PEA3_MOUSE	PAQTGPGQVS	ASARGPGVA	GCSGRMERN	KGYL---	DQ	KVPTTFCSE

SEQ ID NO: 2		110	120	130	140	150
HPPD_Hv	LGAPLAARSD	LSTGSAHAS	QLLRSGHAF	LFT--APTAN	G-CDAA---	
HPPD_Ath	LGMFPAKSD	LSTGMVHAS	YLLTSGDLRF	LFT--APTSP	S--LSAGEIKP	
HPPD_HUMAN	MGFEPLAYRG	LETGSRVVS	HVIRGKIVT	VLS--SA---	---	LNP
HPPD_RAT	MGFEPLAYRG	LETGSRVVS	HVIRGKIVT	VLC--SA---	---	LNP
HPPD_PIG	IGFEPLAYRG	LETGSRVVS	HVIRGKIVT	VFS--SA---	---	LNP
HPPD_MOUSE	MGFEPLAYRG	LETGSRVVS	HVIRGKIVT	VLC--SA---	---	LNP
HPPD_PSESP	PIFINGPTK	VATHRSKDV	ELYRQGANL	ILN--SB---	---	
MELA_SHECO	KVFIDPGPSK	LKKHKQNDI	VYTRQNDIM	LLN--NE---	---	
PEA3_MOUSE	PGNGSLGRAL	MVPGKLMDF	GELPSSDSF	LPQOLSHQF	TWLAEQVDF	

SEQ ID NO: 2		160	170	180	190	200
HPPD_Hv	--TASLPSFS	ADAARRPSAD	HGIAVRGVAL	RVADAAEAFR	ASRRGRARPA	
HPPD_Ath	TTTASLPSFD	HGSCRFPS	HGLGVRAVAI	EVEDARSAFS	ISVARGAIPS	
HPPD_HUMAN	---WN	KEMGDHL-VK	HGDGVKDIAF	EVEDCDIIVQ	KARERGAKIM	
HPPD_RAT	---WN	KEMGDHL-VK	HGDGVKDIAF	EVEDCEHIVQ	KARERGAKIV	
HPPD_PIG	---WN	KEMGDHL-VK	HGDGVKDIAF	EVEDCDIIVQ	KARERGAKIV	
HPPD_MOUSE	---WN	KEMGDHL-VK	HGDGVKDIAF	EVEDCDIIVQ	KARERGAKIV	
HPPD_PSESP	---P	HVASTFAAE	HGPSVCGMAF	RVEDSQKATK	RALELGAQFI	
MELA_SHECO	---K	QGFSAQFAKT	HGPAISSEMN	HVEDANFAFE	GAVARGAKPA	
PEA3_MOUSE	SDEQTVDFPM	---SENLAFF	SPTRIKKFP	QSPRTOPALS	CSKQVPLPYH	

SEQ ID NO: 2		210	220	230	240	250
HPPD_Hv	FAPV---	---DLGRG	FAPAKVELYC	---DVVLRFVS	HP--DG--TD	
HPPD_Ath	SPPI---	---VLREA	VFLAEVELYC	---DVVLRIYS	YKAEOT--SK	
HPPD_HUMAN	REF---	---WVEQDKPK	VKFAVLQTYG	---DTTHZLVE	KIM--YT	
HPPD_RAT	REF---	---WVEQDKPK	VKFAVLQTYG	---DTTHZLVE	KIM--YT	
HPPD_PIG	REHVC-CAAD	VRGHTPLDR	AR---QVME	---GT---LVE	KMT--FC	
HPPD_MOUSE	REF---	---WVEQDKPK	VKFAVLQTYG	---DTTHZLVE	KIM--YT	
HPPD_PSESP	HI---	---ETGPM	LHLPAIKGIG	---GAPFLID	RFSGSSSIYD	
MELA_SHECO	AD---	---EV---KD	LFTPAITYGIG	---DGLIYFID	TFGDDHNIYT	
PEA3_MOUSE	HGEQCLYSRQ	IAIKSPAPCA	PGQSFLQPPS	RABQQQLLR	ASSSSQSHPG	